Data 583 Life Expectancy (WHO)

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22 Mar, 2023

Data 583 Life Expectancy - Final Report (Life Expectancy Data)

1. Introduction and Hypotheses

Life expectancy has always been an area of interest for humanity. The key to long live has remained an intriguing topic to people for decades. The goal of this project is to study a dataset that contains information on life expectancy and identify some of the variables that significantly impact life expectancy.

The dataset chosen for the study has life expectancy data of 193 countries between 2000-2015, together with different predictive factors. Broadly speaking, predicting variables are categorized into 4 major areas : Immunization, Mortality, Economical, and Social, containing a total of 21 individual variables. Our hypothesis is that a subset of variables from this dataset would be able to explain and predict life expectancy with good accuracy (say > 80%). The dataset has a mix of variable types – continuous and discrete. Within discrete types, some variables are ordinal, and some are non-ordinal or nominal.

With such a mix and complexity of data, we also hypothesize that all variables will not share a simple linear relationship with the predictor variable and modelling of life expectancy will require a more complex model. We analyze and validate several statistical models throughout the report with the primary goal of identifying an adequate model for the dataset.

2. Dataset overview

Variables Summary and Categories

Life expectancy is the response variable in this dataset. This represents the mean life expectancy (in age) by specific country and year combination. Refer Figure-1 below for the list of predictor variables and their categories.

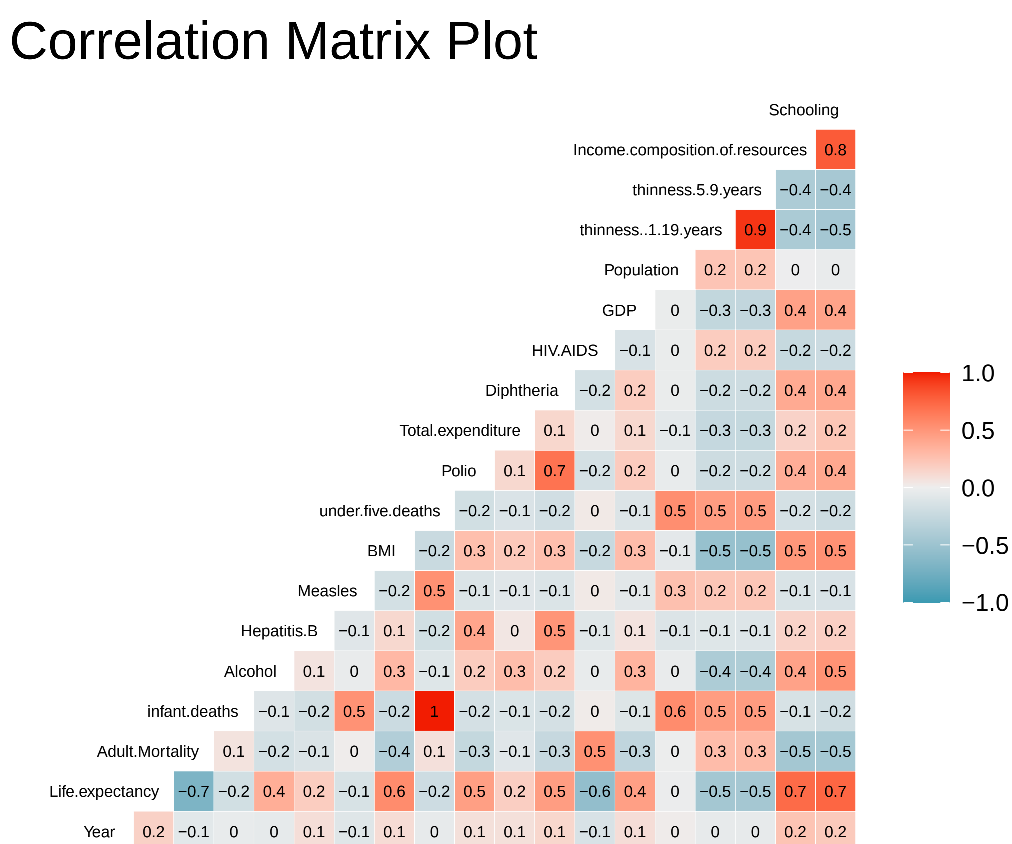
The dataset contains 2563 missing values in various columns. To handle the NA values in the dataset, two main procedures are taken. Firstly, those countries with many NA values in different columns have their records removed from the dataset. Consequently, 12 countries are removed from the dataset. Secondly, the remaining records are imputed by the respective column mean.

To begin with, the 'Percentage expenditure' variable is removed from the entire assessment as the values present in this column are unclear. Another variable 'country' is also removed because we intend to focus on studying the life expectancy on a global basis. The resulting dataset are then studied more closely to understand their correlation effects with the response variable life expectancy.

Variable	Unit of Measurement/Data Category	Continuous vs Discrete	Variable	Unit of Measurement/Data Category	Continuous vs Discrete
Life Expectancy	Years Old (Age)	Continuous	Total expenditure	Percentage	Continuous

Variable	Unit of Measurement/Data Category	Continuous vs Discrete	Variable	Unit of Measurement/Data Category	Continuous vs Discrete
Country	Nominal Data	Discrete	Percentage expenditure	Percentage	Continuous
Year	Ordinal Data	Discrete	GDP	Currency (USD)	Continuous
Status	Nominal Data	Discrete	Population	Count	Discrete
Adult Mortality	Count Data	Discrete	Income composition of resources	Percentage	Continuous
Infant deaths	Count Data	Discrete	Schooling	Mean (Years)	Continuous
Under-five deaths	Count Data	Discrete	Alcohol	Litres	Continuous
Hepatitis B	Percentage	Continuous	HIV/AIDS	Percentage	Continuous
Measles	Count Data	Discrete	BMI	Average BMI	Continuous
Polio	Percentage	Continuous	Thinness 1-19 years	Percentage	Continuous
Diphtheria	Percentage	Continuous	Thinness 5-9 years	Percentage	Continuous

Figure 1 : List of Predictor Variables



Plot 1 : GG Variables Correlation Plot

Initial analysis using linear regression

Life expectancy is a continuous variable and the first choice is building a linear regression model which is simple and interpretable. A BIC backward step model variable selection method is also applied on the full model to arrive at a parsimonious model containing only significant predictor variables. Following table Table A provides a summary of the two models.

Models	No. of Variables	AIC Score	Adj R-squared Score
Original Model	20	7642.14	0.8299
Reduced Model	12	7604.24	0.8296

Figure 2 :Original vs Reduced Models

Note that we have also eliminated the Status variable in the reduced model as this is a factor variable with two statuses and not continuous. We plan to first study the effect of the model without this variable. Finally, the number of independent variables is now effectively reduced to 12, maintaining a AIC score of 7604.34. Meanwhile, the adjusted R-squared score is well kept at nearly the same level as in the original model. The reduced model is able to explain more than 82% of variation in the response variable and its performance is above the anticipated 80%.

Specifically, the reduced model now contains the following 12 variables : Adult.Mortality + infant.deaths + Hepatitis.B + BMI + under.five.deaths + Polio + Diphtheria + HIV.AIDS + GDP + thinness..1.19.years + Income.composition.of.resources + Schooling. To conclude, the resulting dataset to be used in the reduced model has 2778 records and 12 columns.

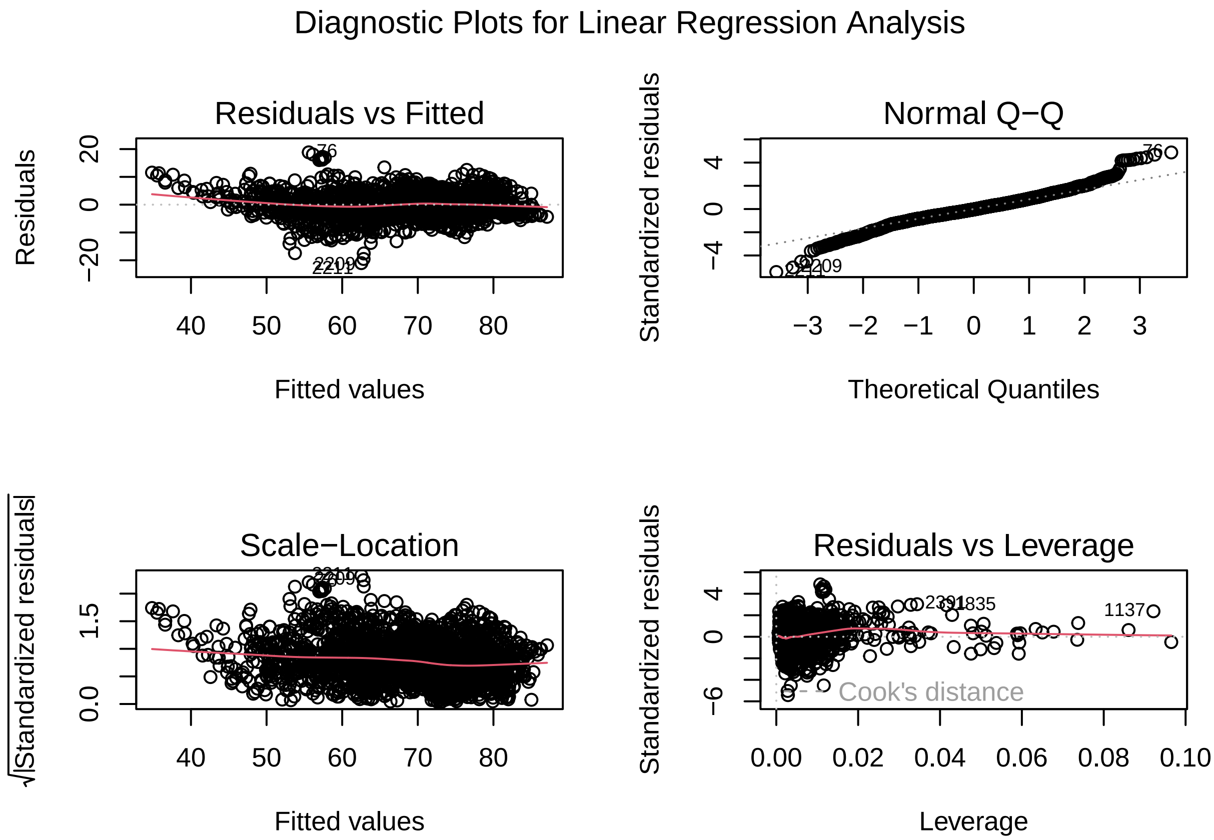
With performance of the model over 80%, the next step is to look at the error diagnostics from the model.

3. Regression Analysis

Linear model and diagnostics

The initial model shows that we are able to explain approximately 82% of variability of our response variable using the selected predictor variables. The next step is to look at the error diagnostics from the model.

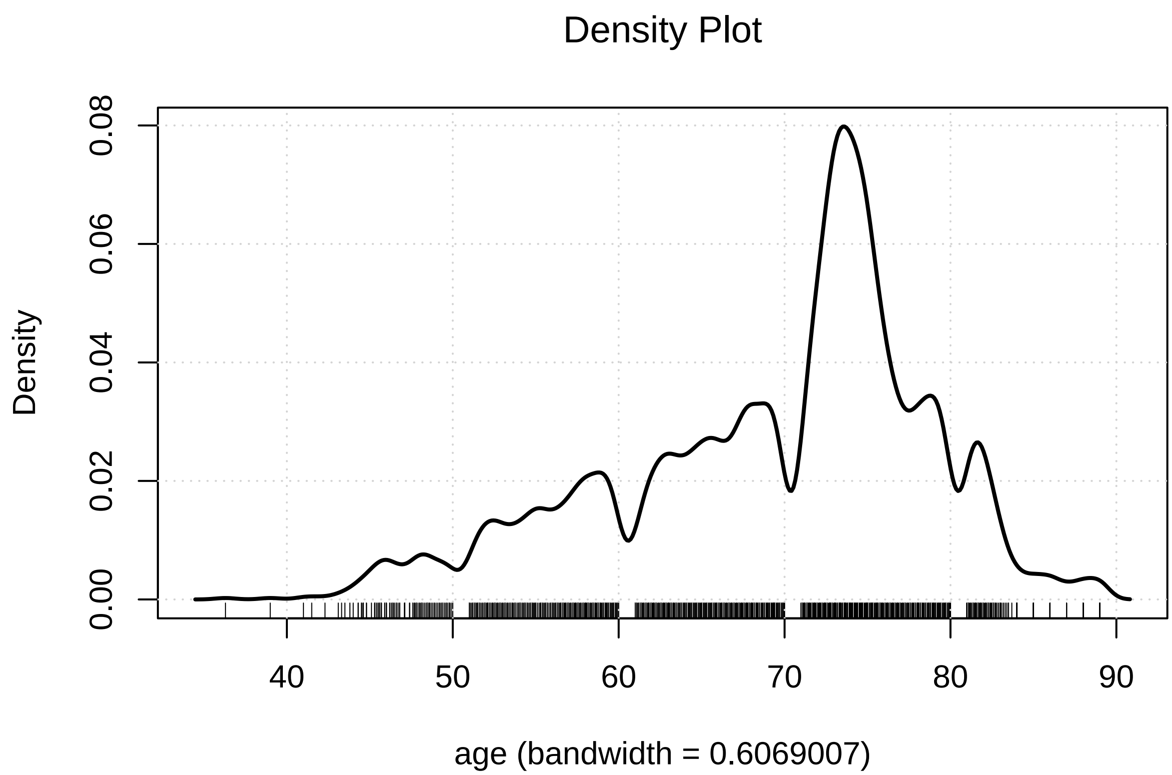
```
par(mfrow=c(2,2))

plot(lmmod2)
mtext("Diagnostic Plots for Linear Regression Analysis", side = 3, line = -1, outer = TRUE)
```



The QQ plot suggests that the model is heavy tailed and the data on both ends of the quantiles do not fit on a straight line. This is an indication that the current linear regression based model is not fitting the data well. Based on this, we undertake some additional testing to validate if the model is adequate and valid.

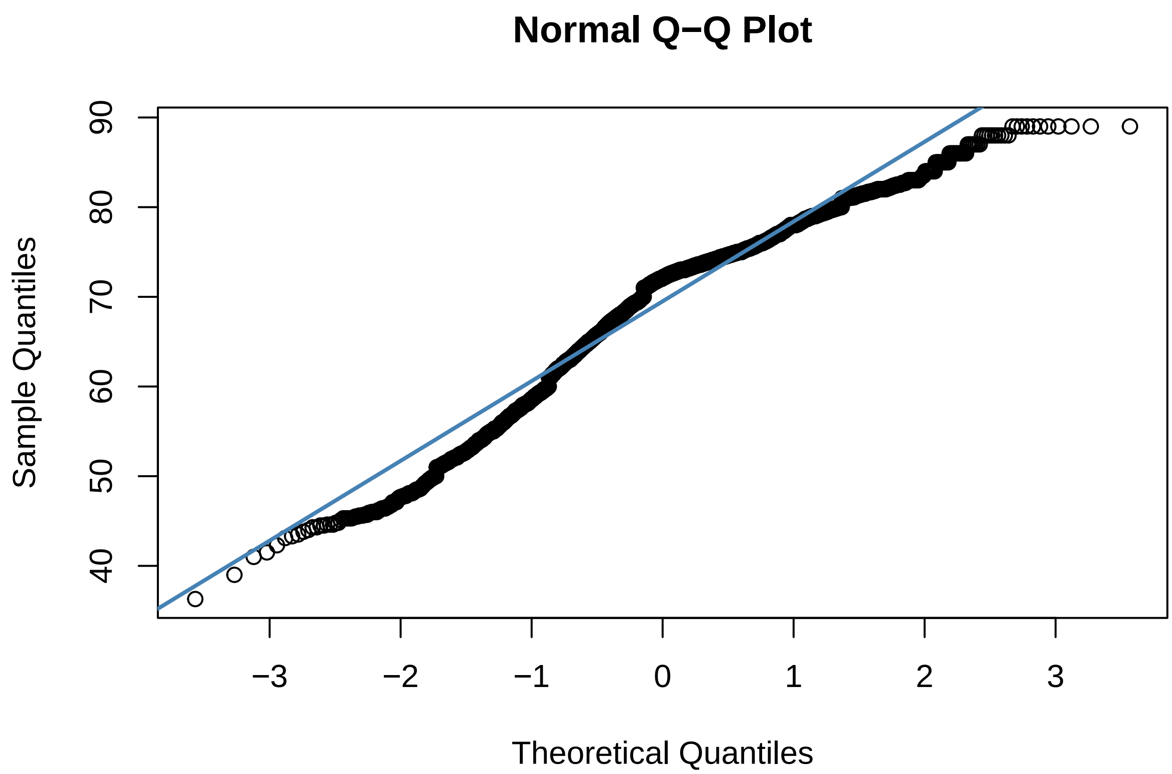
```
densityPlot(~ Life.expectancy, show.bw=TRUE, method="kernel", data = df, xlab="age")
title(main="Density Plot",font.main= 1)
```

a. Life expectancy variable distribution



From the Density plot above, we can see that the mean the distribution isn't symmetrical and the mean isn't centered at 0, indicating the response variable life expectancy is not normally distributed. The distribution also seems to have a 2nd peak indicating our response variable have a bimodal distribution.

```
qqnorm(df$Life.expectancy)
qqline(df$Life.expectancy, col = "steelblue", lwd = 2)
```




```
# plot(lmmod2,which = 2)
#Both are indicating that our predict variable Y "df$Life.expectancy" is not normally distributed
```

From the Normal QQ plot, we could see that there is distinct curve in the middle of plot rather than a having a straight line, this suggest us that there is a bimodal distributions to our response variable.

b. Normal distribution test for our y variable Next, we evaluate to confirm if the response variable is normally distributed using Shapiro-Wilk test. The test has a p-value that is very small and is less than 0.05, this indicates that our response variable if not normally distributed.

```
#Shapiro-Wilk Test

shapiro.test(df$Life.expectancy)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df$Life.expectancy
## W = 0.95676, p-value < 2.2e-16
```

```
#Finding: Since df$Life.expectancy p-value is less than .05, indicate that our y variable is not normally
```

As response is not normal, the next step is to validate with a hypothesis test for validating correct specification of parametric MLR models.

c. Parametric model specification test Another test to see if the above parametric model specification is correct.

```
library(lmtest)
```

```
## Warning: package 'lmtest' was built under R version 4.2.2

## Loading required package: zoo

## Warning: package 'zoo' was built under R version 4.2.2

##
## Attaching package: 'zoo'

## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
resettest(lmmod2)
```

```
##
##  RESET test
##
## data:  lmmod2
## RESET = 121.2, df1 = 2, df2 = 2763, p-value < 2.2e-16
```

d. Consistent nonparametric inference

```
##
## Consistent Model Specification Test
## Parametric null model: lm(formula = Life.expectancy ~ Adult.Mortality +
##                           infant.deaths + Hepatitis.B + BMI + under.five.deaths
##                           + Polio + Diphtheria + HIV.AIDS + GDP +
##                           thinness..1.19.years +
##                           Income.composition.of.resources + Schooling, data =
##                           df, x = TRUE, y = TRUE)
## Number of regressors: 12
## IID Bootstrap (399 replications)
##
## Test Statistic 'Jn': 21.17521    P Value: < 2.22e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Null of correct specification is rejected at the 0.1% level
```

All the diagnostic tests indicate that linear regression is not an appropriate model for the given data as assumptions for the model are violated.

Parametric regression models and relative assessments

As the linear model is not adequate, we move on to model this with other models that do not assume normal distribution. The models selected for the given dataset are LASSO and Neural Net with linear activation function. The following variables are selected for rest of the modeling based on correlation of the variables with the response variable and our knowledge on the domain. Here is a summary of the variable selection and our comments.

Data Categories	Vaiables
Economical Data	Total expenditure, Percentage expenditure, GDP, Income composition of resources
Social Data	Country, Status, Population, Schooling, Alcohol, BMI, Thinness 1-19 years, Thinness 5-9 years
Mortality Data	Adult Mortality, Infant deaths, Under-five deaths
Immunization Data	Hepatitis B, Measles, Polio, HIV/AIDS, BMI, Diphtheria

Column Name	Type	LM	LASSO	NN	NPREG	Reason of Removal
Country	(Discrete)					Since we wanted to build models for all countries
Year	(Discrete)					ordinal type data and based on domain knowledge, not consider important
Status	(Discrete)					nominal type data and based on domain knowledge, not consider important
Adult Mortality	(Discrete)	X	X	X	X	
Infant deaths	(Discrete)	X	X	X	X	
Under-five deaths	(Discrete)	X	X	X	X	
Hepatitis B	(Continuous)	X	X	X	X	
Measles	(Discrete)					Since it is a count and discrete type data and weak correlation with our predictor
Polio	(Continuous)	X	X	X	X	
Diphtheria	(Continuous)	X	X	X	X	
Total Expenditure	(Continuous)					based on domain knowledge, not consider important
Percentage Expenditure	(Continuous)					based on domain knowledge, not consider important
GDP	(Continuous)	X	X	X	X	
Population	(Discrete)					no correlation with our predictor indicated by our correlation plot
Income composition of resources	(Continuous)	X	X	X	X	
Schooling	(Continuous)	X	X	X	X	
Alchol	(Continuous)					based on domain knowledge, not consider important
HIV/AIDS	(Continuous)	X	X	X	X	
BMI	(Continuous)	X	X	X	X	
Thinness 1-19 years	(Continuous)	X	X	X	X	
Thinness 5-9 years	(Continuous)					range already covered in 1-19 Thinness 1-19 years
status.val	(Continuous)					based on domain knowledge, not consider important

Two different supervised algorithms tried on the dataset. They do not have the constraint of a normal distribution for response variable.

First did a train and test split so we can measure the MSE and compare how each of the models are performing in terms of minimizing MSE.

PRESS comparison for the three models

	LM	LASSO	NN
PRESS	15.93367	15.98972	22.43056

Test R2 comparison for the three models

	LM	LASSO
R2	0.829139273435324	0.829061931452822

As we compare linear model, lasso and neural net, we see that the test MSE is minimum for LASSO model. So this is a model that can be considered for the dataset.

Diagnostics

Nonparametric regression

The response variable shows a bimodal distribution and nonparametric regression performs better on such datasets per literature. We next try non parametric regression on the dataset.

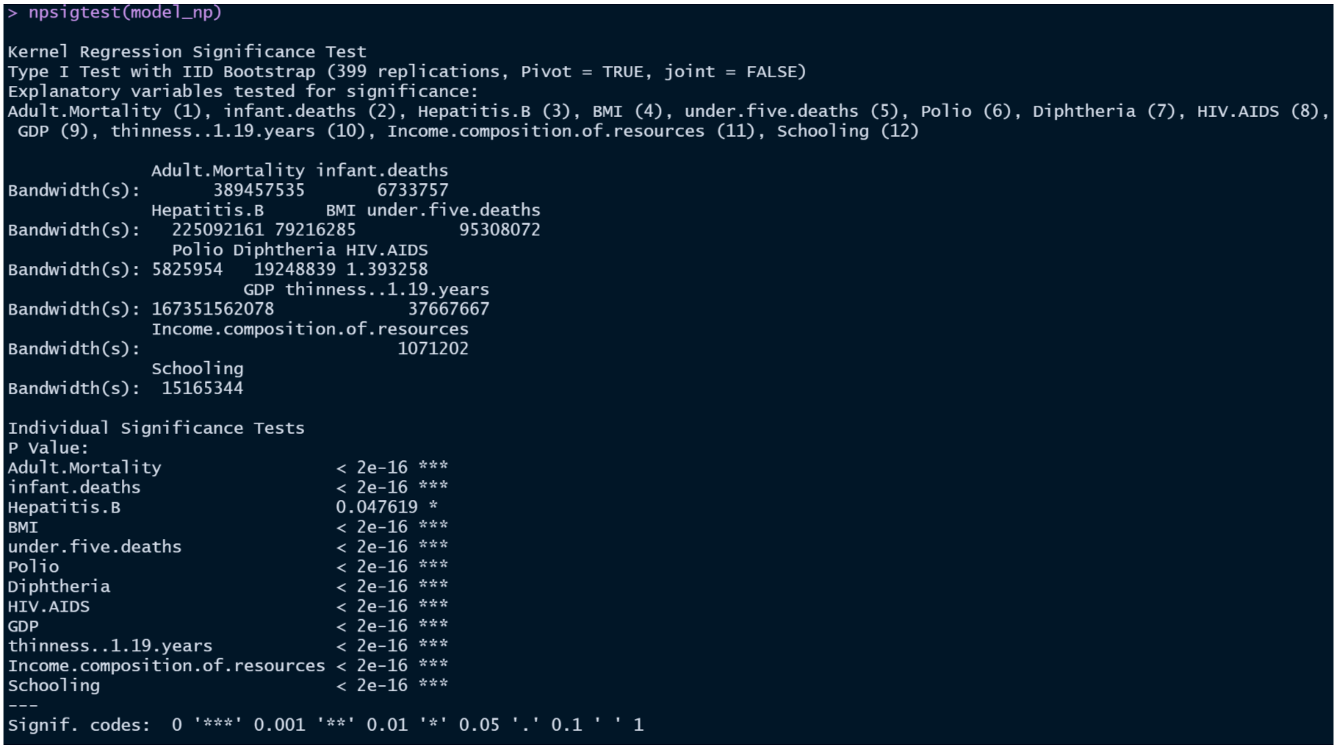
```
library(np)
# n <- names(df)
# f <- as.formula(paste("df$Life.expectancy ~", paste(n[!n %in% "Life.expectancy"], collapse = " + ")))
#
# model_np <- npregbw(Life.expectancy ~ Adult.Mortality + infant.deaths + Hepatitis.B + BMI + under.five.d

# model_np <- npreg(bws = model_np)
# summary(model_np)
model_np <- readRDS("model_np.rds") #PreTrained Model
summary(model_np)
```

Diagnostics

```
##
## Regression Data: 2778 training points, in 12 variable(s)
##               Adult.Mortality infant.deaths Hepatitis.B      BMI
## Bandwidth(s):       389457535       6733757   225092161 79216285
##               under.five.deaths   Polio Diphtheria HIV.AIDS          GDP
## Bandwidth(s):          95308072 5825954   19248839 1.393258 167351562078
##               thinness..1.19.years Income.composition.of.resources Schooling
## Bandwidth(s):             37667667                         1071202  15165344
##
## Kernel Regression Estimator: Local-Linear
## Bandwidth Type: Fixed
## Residual standard error: 3.345092
## R-squared: 0.8722143
##
## Continuous Kernel Type: Second-Order Gaussian
## No. Continuous Explanatory Vars.: 12
```

We see that the R^2 is increased to 87% approximately. Done with local linear estimator and cv.aic. This is a cross validated model and help estimate the long run performance. Can we see BIC?

```r
#npsigtest_npreg <- npsigtest(model_np)    #10 HRs to run...
```



```
> npsigtest(model_np)

Kernel Regression Significance Test
Type I Test with IID Bootstrap (399 replications, Pivot = TRUE, joint = FALSE)
Explanatory variables tested for significance:
Adult.Mortality (1), infant.deaths (2), Hepatitis.B (3), BMI (4), under.five.deaths (5), Polio (6), Diphtheria (7), HIV.AIDS (8),
 GDP (9), thinness..1.19.years (10), Income.composition.of.resources (11), Schooling (12)

              Adult.Mortality infant.deaths
Bandwidth(s):       389457535       6733757
              Hepatitis.B      BMI under.five.deaths
Bandwidth(s):   225092161 79216285          95308072
                Polio Diphtheria HIV.AIDS
Bandwidth(s): 5825954   19248839 1.393258
                       GDP thinness..1.19.years
Bandwidth(s): 167351562078             37667667
              Income.composition.of.resources
Bandwidth(s):                         1071202
              Schooling
Bandwidth(s):  15165344

Individual Significance Tests
P Value:
Adult.Mortality                 < 2e-16 ***
infant.deaths                   < 2e-16 ***
Hepatitis.B                     0.047619 *
BMI                             < 2e-16 ***
under.five.deaths               < 2e-16 ***
Polio                           < 2e-16 ***
Diphtheria                      < 2e-16 ***
HIV.AIDS                        < 2e-16 ***
GDP                             < 2e-16 ***
thinness..1.19.years            < 2e-16 ***
Income.composition.of.resources < 2e-16 ***
Schooling                       < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 1: npsigtest_npreg result

We measure the significance of the variables for a parsimonious model. All the parameters used are significant.

Summarizing the different models and the performance assessed during the course of this project

	NPREG	**LASSO**
R2	0.8722143	0.829061931452822

4. Model Improvements

While a number of different models and statistical tests have been explored within a limited time frame of this project, we can hardly conclude we have identified the globally optimal models. In fact, in order to limit the complication of this analysis and make it reasonably achievable, we have adopted certain model and analysis simplification in a few aspects. These assumptions/simplification may, however, potentially have adverse effect on our underlying models accuracy. As rooms of further improvement works based on this report, the following aspects are suggested for future exploration, studies and implementation to see if an even better-performing model can be attained.

1. Currently, no particular handling has been done to process the categorical, ordinal, and nominal variables. Current variables are simply fit into different models with "as-is" data basis. Further exploration on whether some techniques (such as Variables Encoding/transformation, factorization factor()) can be deployed to achieve models improvement is preferable.

2. Performing non-parametric model in our analysis has taken a substantial amount of computing resources. The studies on the non-parametric model what we have achieved so far is generally sufficient for measuring long run performance. While resources and time allow in the future, we may consider performing further fine-tuning on this by enforcing dataset splitting into training and testing set under non-parametric model fitting, which can possibly have a better account of the model performance.

3. According to the earlier Multicollinearity studies (Part 2), correlation is found between the variables infant.deaths and under.five.deaths. It is understood that such correlation may cause undesirable effect on model accuracy, fitting and interpretation. To resolve this issue, we may explore possible tactics such as removing one of the correlated variables, or using factor analysis (factanal) to address the multicollinearity issue to enhance the models.

4. Currently in our analysis, data implantation (rather than removing the records with NA values) has been deployed in order to retain as many records as possible and simplify/streamline the subsequent analysis. Although data implantation is a common industry practice, We are not 100% sure if such procedure would affect the model accuracy. In this regard, we may investigate and compare different null data handling techniques (apart from data implantation using mean) and investigate if we can achieve our modelling improvement as a result.

5. Challenges

During this project, a number of challenges are encountered. These challenges have created extra hurdles and unforeseeable overheads on our projects, or have caused unexpected complication for the project team in order to efficiently and confidently identify the most suitable models.

1. Running npreg on our model is extremely time-consuming. It took 30 hours in a notebook computer. This undesirable situation has seriously constrained our flexibility in fine-tuning and re-running the model with different model settings such as variable combination because we simply cannot afford adjusting the model fitting to look more a potentially more optimal model fitting.

2. Similarly, running model significance took more than 30 hours. This has caused similar consequence as the previous point 1.

3. As mentioned in the earlier analysis, bimodal distribution is identified in the dataset, which has violated the basic assumptions of many parametric models. This behavior has therefore severely limited the applicability of many parametric modelling. We also lack of sufficient knowledge on how to optimally model and analyze bimodal distribution.

4. The dataset has demonstrated quite a high proportion of NA values. Several columns contain significantly more than 5% of NA values. If we decide to adopt the 5% threshold and remove all records (e.g. dropping columns or removing rows) with NA values which exceeds the 5% threshold, it would result in a significant amount of records being removed and only remain a much smaller sample size available for further analysis. This may tremendously and adversely impact and deteriorate the analysis accuracy and reliability.

6. Conclusion

The non-normality nature of the dataset has been observed and verified by rigorous testings and validation in this report. This characteristic has greatly limited the applicablity of many popular common models which rely on the assumption of normal distribution. After further model assessment, we are finally able to come into the best available conclusion that NOREG and LASSO are the two best-performing models based on model performance indicators like MSE and R-squared values.

We find that life expectancy is….[KT : I literally have no idea what to put there….may be I leave it to Viji to continue and finally conclude the report :)]

Appendix

Checking for Multicollinearity

As Multicollinearity can potentially affect the accuracy of regression model and we have 22 variables, a correlation study is undertaken to understand and assess the situation. A correlation plot has identified a number of correlation problems. It is found that infant deaths and under.five.deaths are nearly 100% correlated. The relation between the deaths rates of the two close age groups is easily interpretable. In addition, there are three heavily correlated pairs which is defined by the abs(correlation coefficient)>0.7 between the variables. They include (a) (immunization rate of) 'Polio'-vs-'Diphtheria', (b) 'income composition of resources'-vs-'Schooling', and (c) between the two thinness measures for the age groups 5-9 vs 10-19. Pairs (a) and (c) are justifiable while the relation for (b) demonstrate a relatively subtle relation. Other than that, the degree of multicollinearity is acceptable and not too worrying.